

Fig. 1

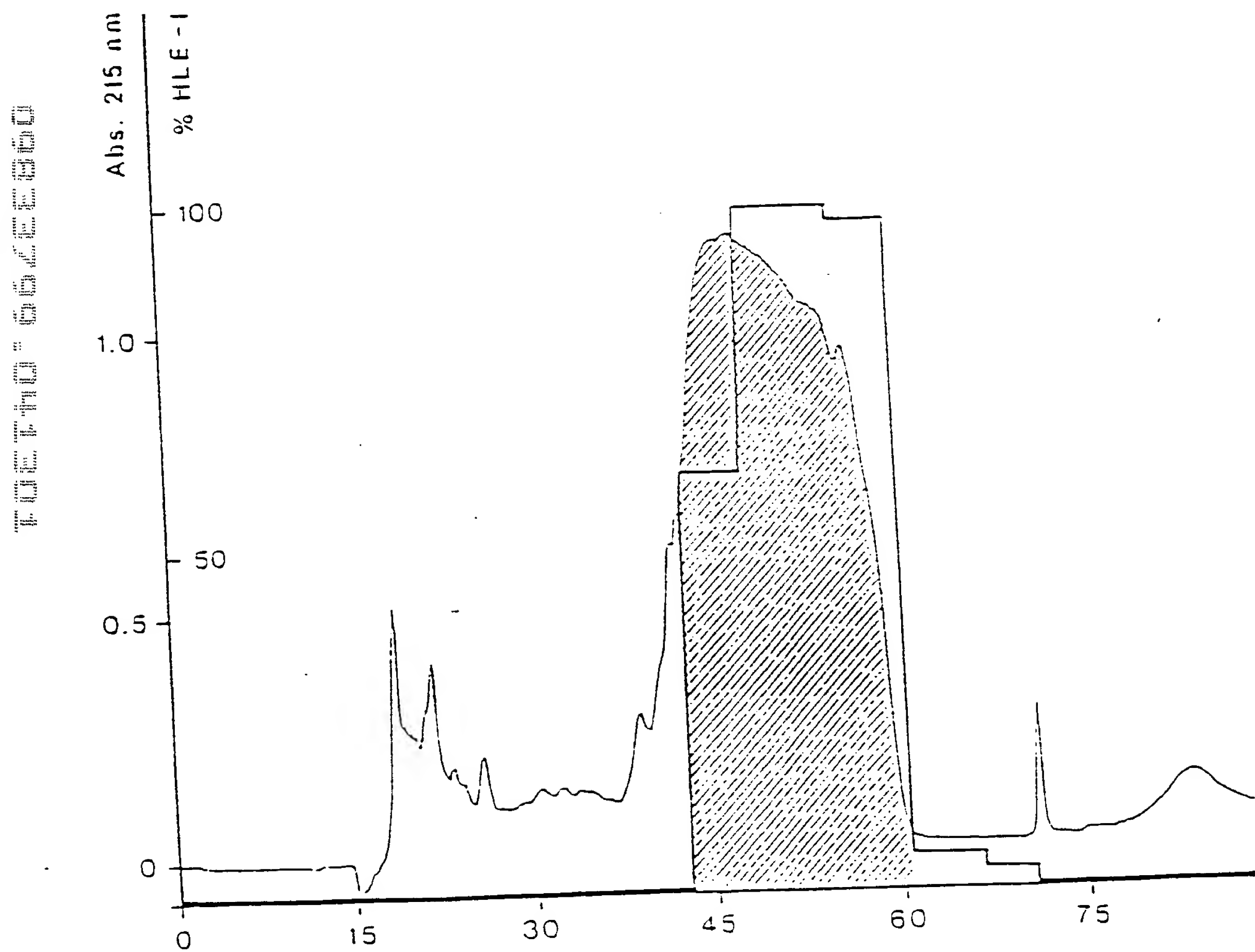


Fig. 2

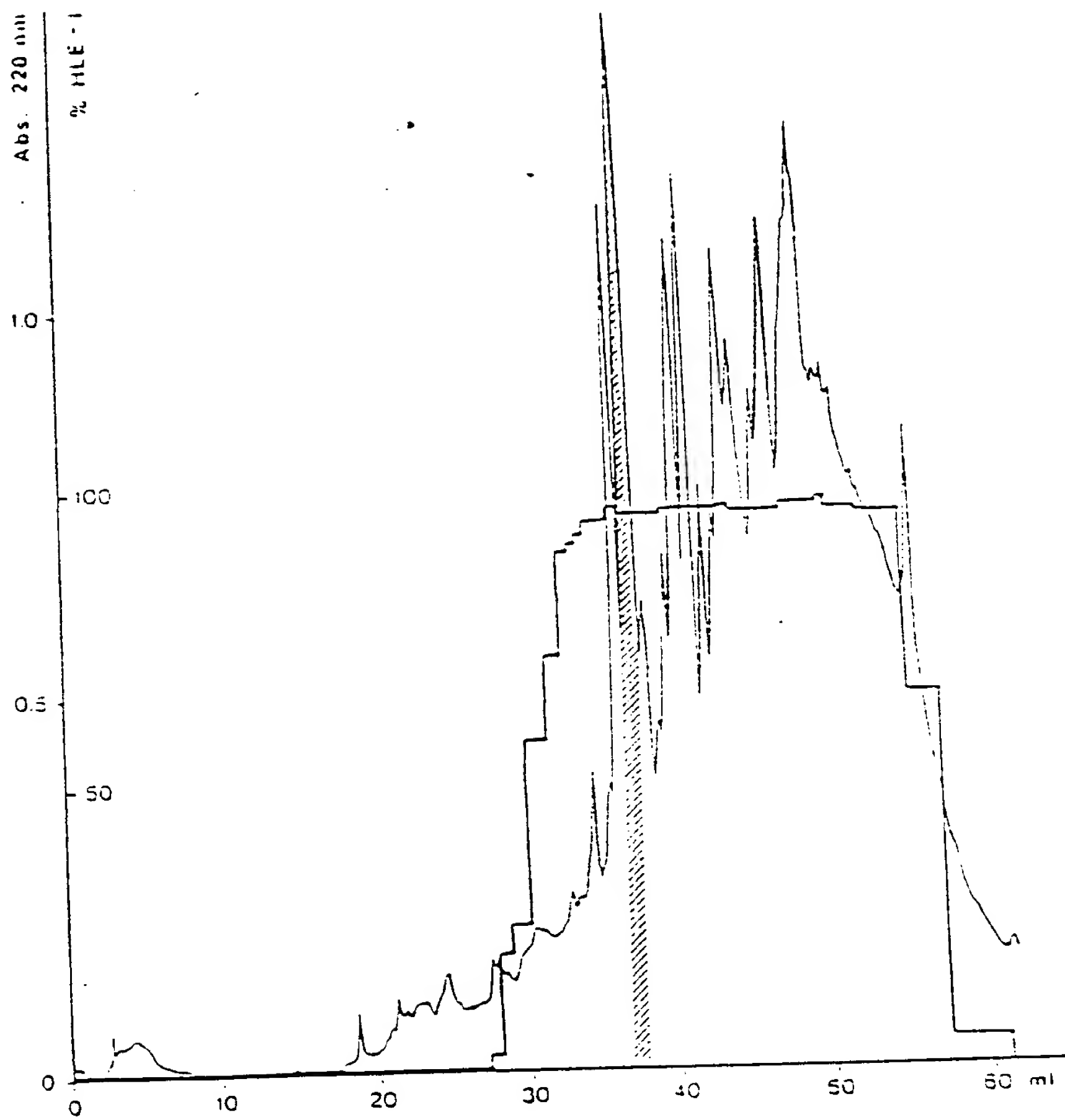


Fig. 3

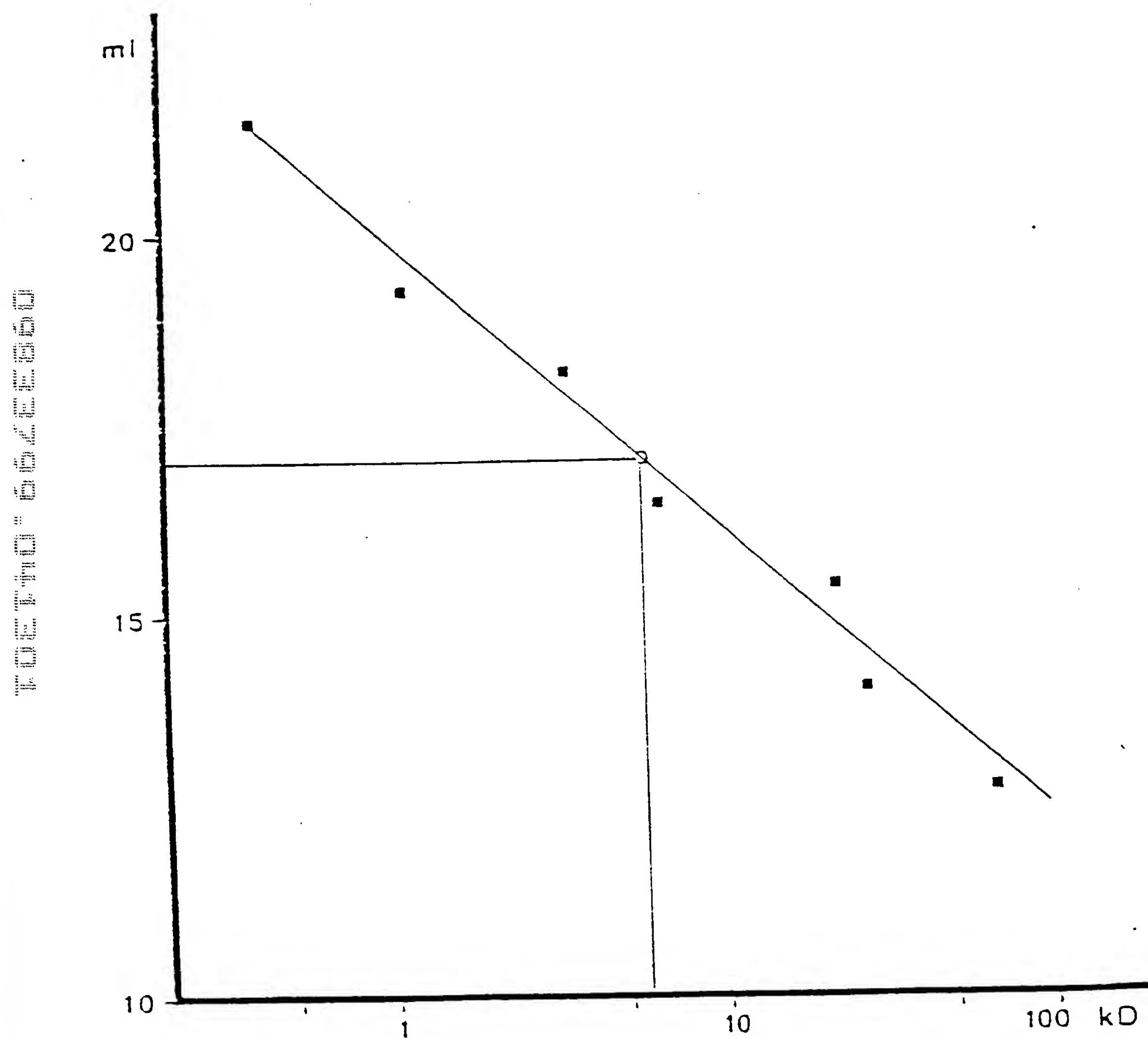


Fig. 5

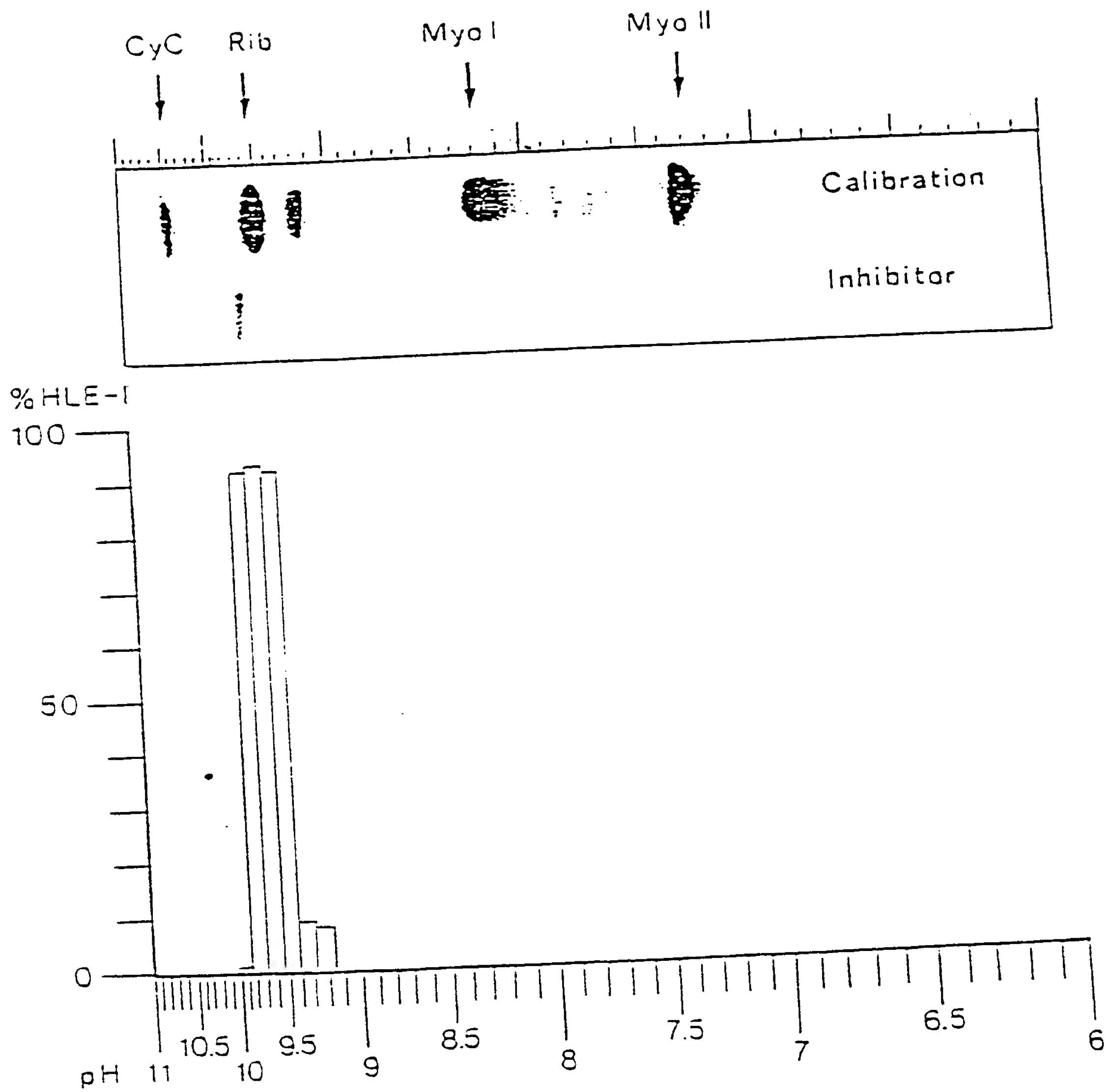


Fig. 6

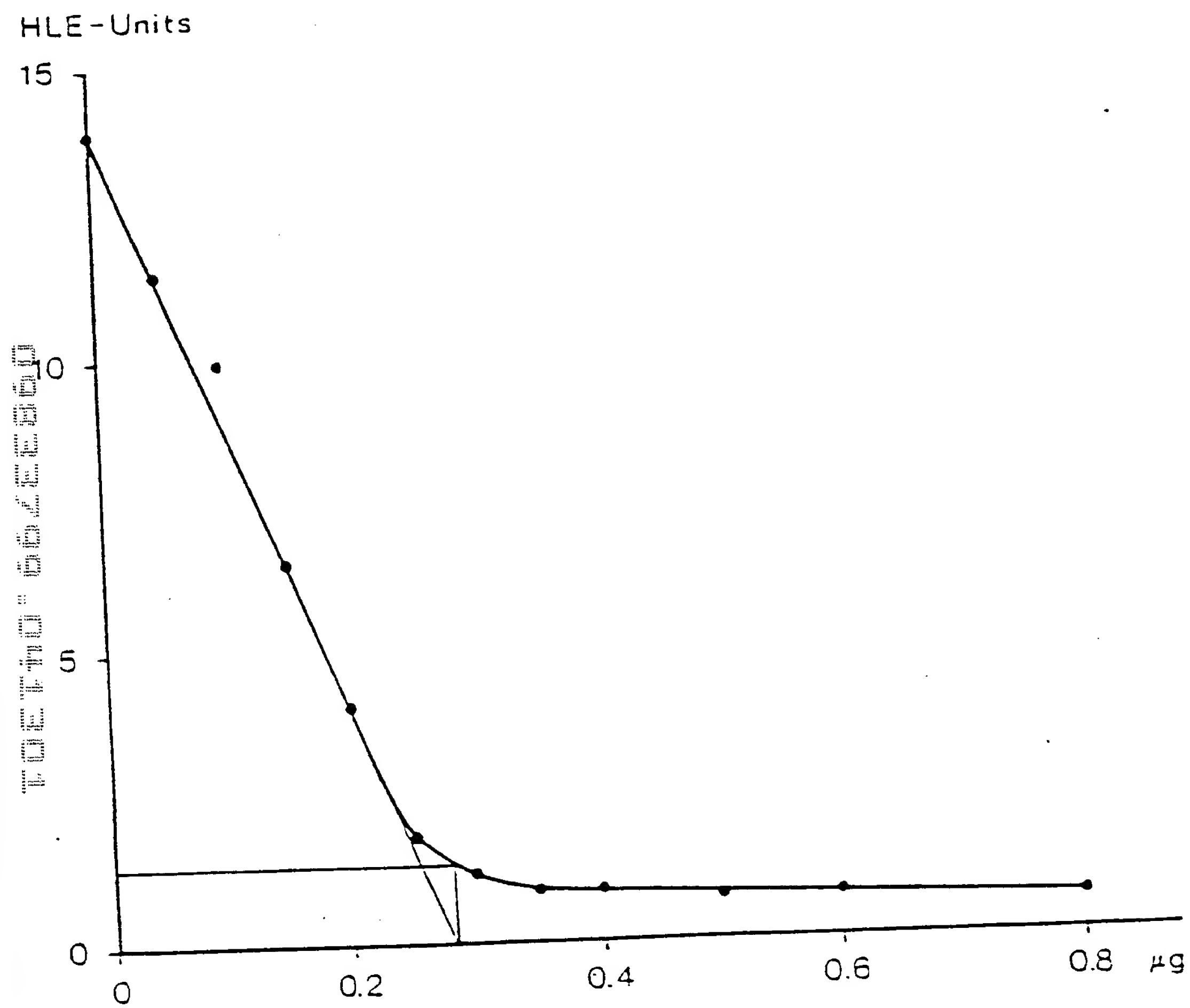


Fig. 7

FIGURE 8

PROTEIN SEQUENCE OF ELASTASE INHIBITOR



X=UNIDENTIFIED T=TRYPTIC FRAGMENTS C=CHYMOTRYPTIC FRAGMENTS

662660

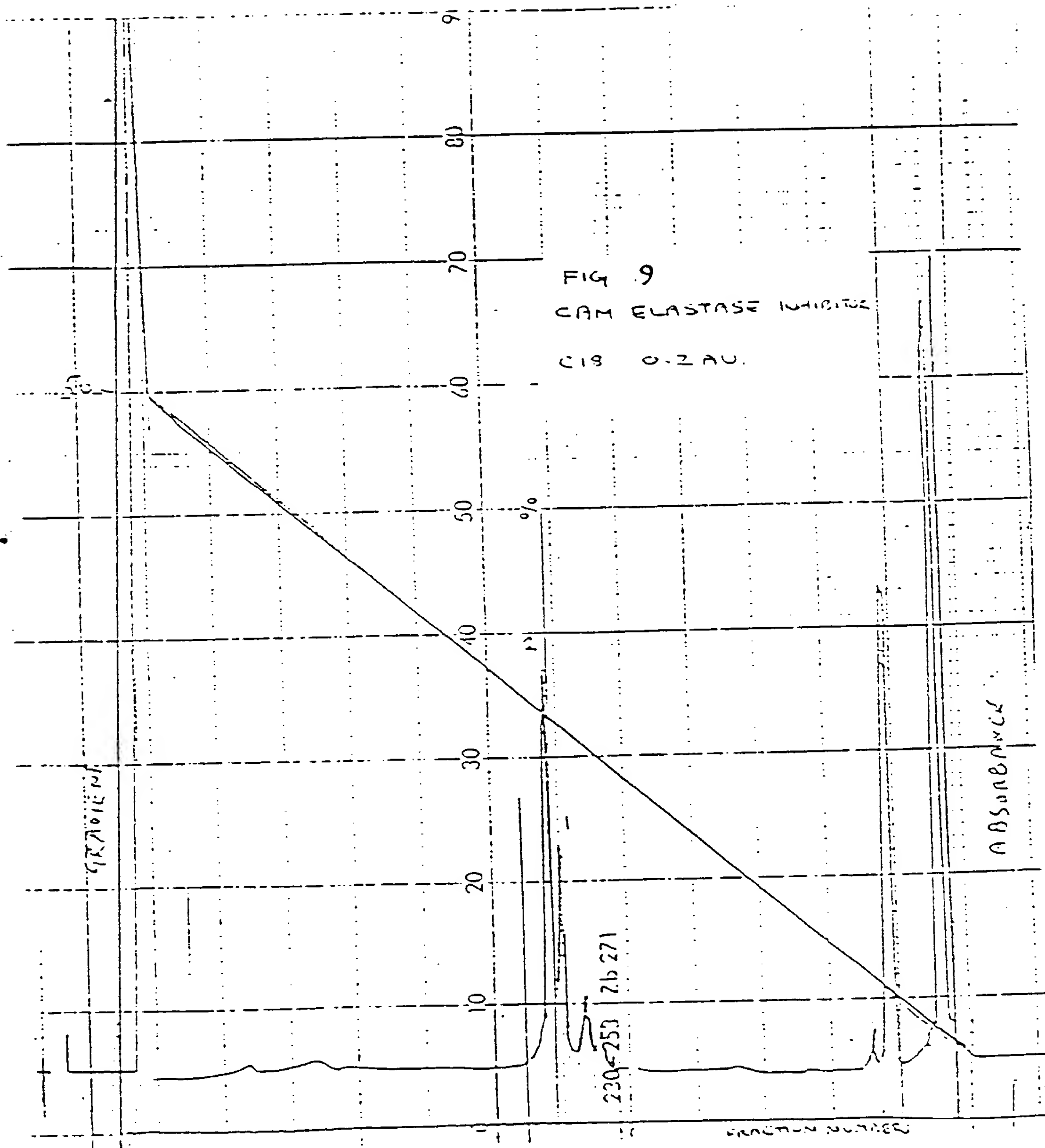
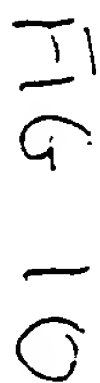


FIG 9.

[illegible]

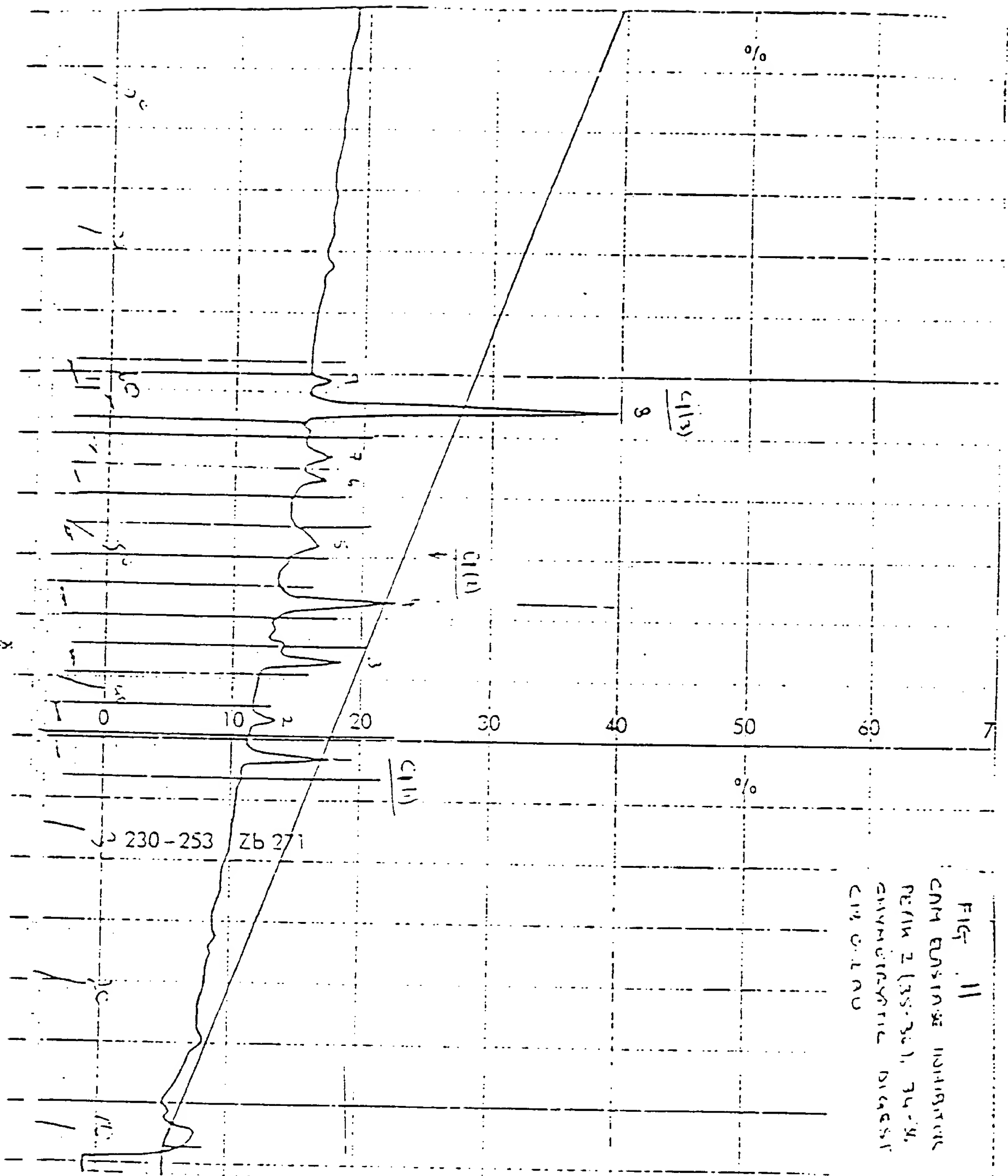


FIG. 11
CUMULATIVE INTENSITY
PEAK 2 (35-36), 34-36,
CHEMICAL DIGEST
CUMULATIVE

FIG 11

FIG. 12
CAM ELASTASE INHIBITOR
(35-36), 34-38
TRYPTIC DIGEST
CIR C.I.N.U.

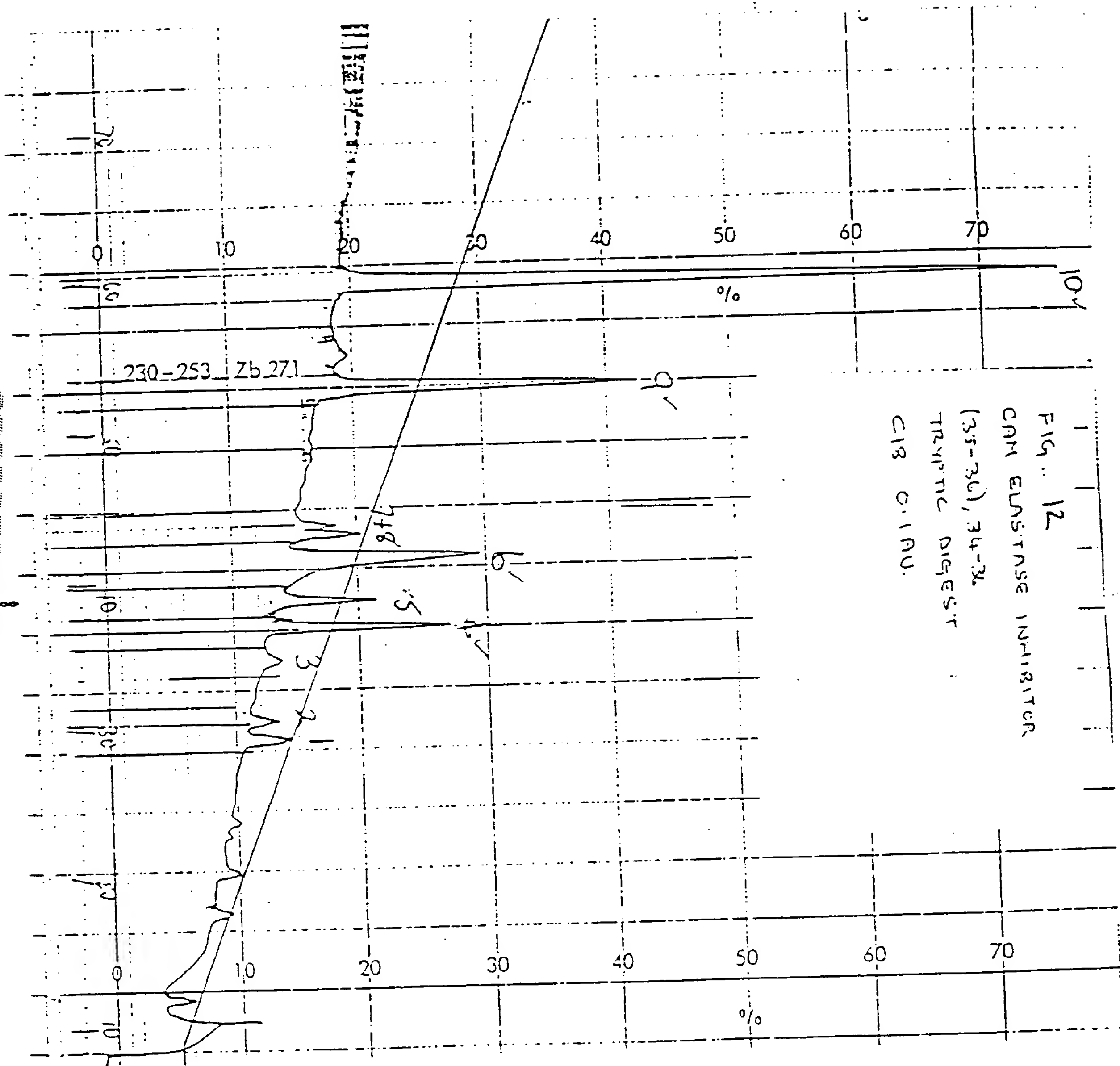



FIG 12

Figure 13

AlaGlnGluProValLysGlyProValSerThr

1  ELI1
AATTCGAGCTCGGTACCATACCTGCATATGCTCAAGAACCAGTTAAAGGTCCTGTGTCTACT
GCTCGAGCCATGGTATGGACGTATACGAGTTCTTGGTCAATTTCCAGGACACAGATGA

LysProGlySerCysProIleIleLeuIleArgCysAlaMetLeuAsnProProAsnArg

63
AAGCCAGGTTCTTGTCTATTATCTTGATTGTTGCGCTATGTTAAACCCACCTAACCGT
TTCGGTCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCA
ELI2 ←

CysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGlySerCysGlyMet

123
TGT TTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTCTGCGGTATG
ACAACTTCCTGTGACTAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATAC
ELI4

AlaCysPheValProGlnEndEnd

183 GCTTGTTTCGTTCCACAATAATAG

CGAACAAAGCAAGGTGTTATTATCCTAG 210

ELI6 ←

Ala Gln Glu Pro Val Lys Gly Pro Val Ser Thr Lys Pro Gly Ser Cys
GCG CAA GAG CCA GTC AAA GGT CCA GTC TCC ACT AAG CCT GGC TCC TGC
5' DNA
Sequence

Leu Lys Asp Thr Asp Cys Pro Gly Ile Lys Lys Cys Cys Glu Gly Ser

Cys Gly Met Ala Cys Phe Val Pro Gln
TGC GGG ATG GCC TGT TTC GTT CCC CAG

P = A or G

Ala Gln Glu Pro Val Lys Gly Pro Val Ser Thr Lys Pro Gly Ser Cys
GCG CAA GAG CCA GTC AAA GGT CCA GTC TCC ACT AAG CCT GGC TCC TGC

5' DNA
Sequence

Pro Ile Ile Leu Ile Arg Cys Ala Met Leu Asn Pro Pro Asn Arg Cys
CCC ATT ATC TTG ATC CGG TGC GCC ATG TTG AAT CCC CCT AAC CGC TGC

Leu Lys Asp Thr Asp Cys Pro Gly Ile Lys Lys Cys Cys Glu Gly Ser

TTG AAA GAT ACT GAC TGC CCA GGA ATZ AAG AAP TGC TGT GAA GGC TCT

Cys Gly Met Ala Cys Phe Val Pro Gln

Cys Gly Met Ala Cys Phe Val Pro Gln
TGC GGG ATG GCC TGT TTC GTT CCC CAG TAG GAGGGAGCCGGTCCTTGCTGCACCTGT

GCGTCCCCAGAGCTACAGGCCCCATCTGGTCCTAAGTCCCTGCTGCCCTTCCCCTTCCCACACTGTCCA
 TTCTTCCTCCCATTCAGGATGCCACGGCTGGAGCTGCCTCTCTCATCCACTTTCCAATAAAGAGTTCCG
 GAATTC

Poly A 3'
signal

Z = T, C or A

P = A or G

10 30 50

GGAATTCCGGTTCCTCATCGCTGGGACGCTGGTTCTAGAGGCAGCTGTCACGGGAGTTCC

EcoRI XbaI

F L I A G T L V L E A A V T G V P

|-----IN-FRAME UPSTREAM PROTEIN SEQUENCE-----

70 90 110

TGTTAAAGGTCAAGACACTGTCAAAGGCCGTGTTCCATTCAATGGACAAGATCCCGTTAA

V K G Q D T V K G R V P F N G Q D P V K

130 150 170

AGGACAAGTTTCAGTTAAAGGTCAAGATAAAGTCAAAGCGCAAGAGCCAGTCAAAGGTCC

G Q V S V K G Q D K V K

AlaGlnGluProValLysGlyPr

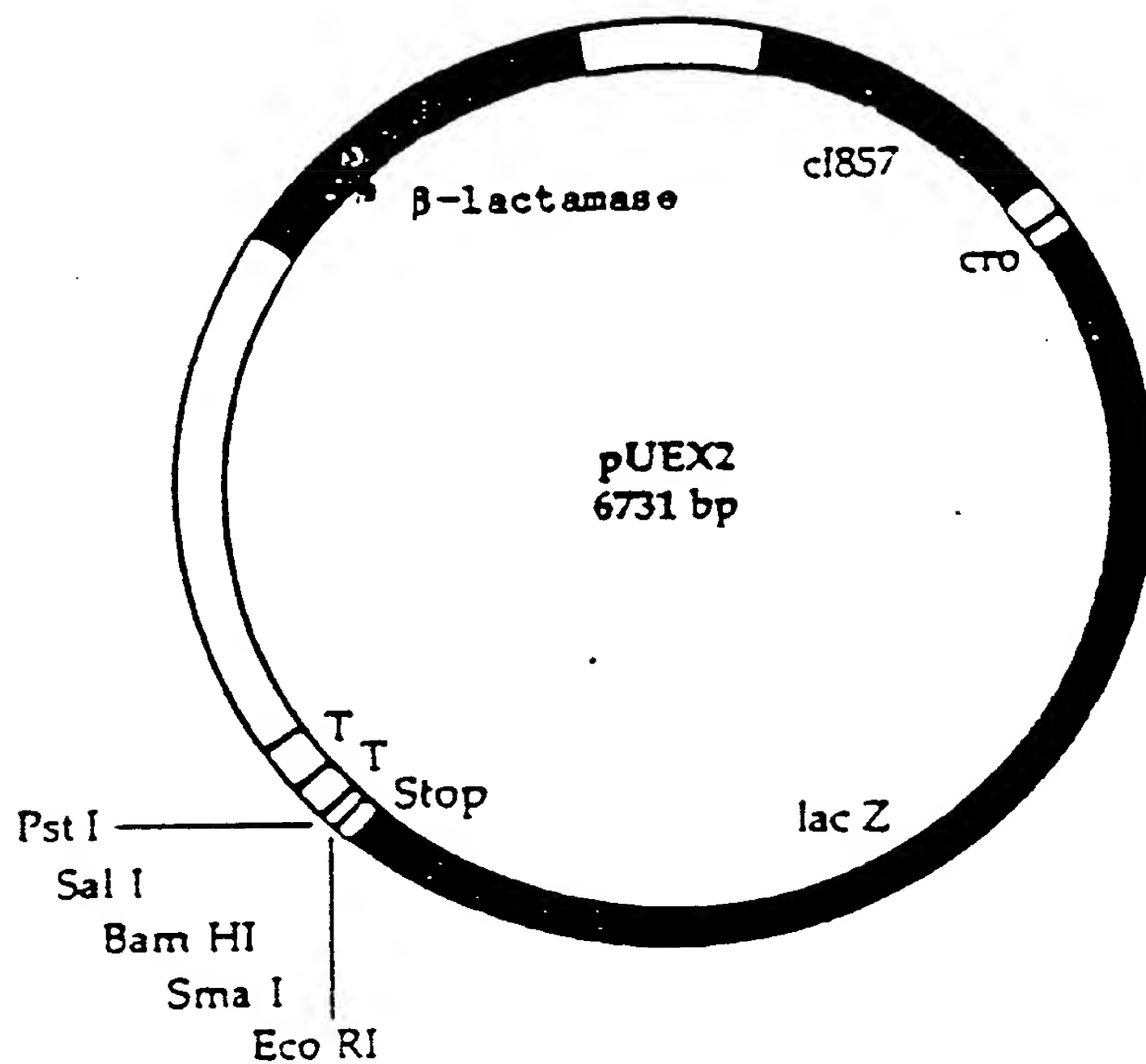
|--ELASTASE INHIBITOR--

Cont'd 16b of 19

FIGURE 16 CONTINUED

190 210 230
 AGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTGATCCGGTGCGCCATGTTGAATCC
 oValSerThrLysProGlySerCysProIleIleLeuIleArgCysAlaMetLeuAsnPr
 250 270 290
 CCCTAACCGCTGCTTGAAAGATACTGACTGCCCAGGAATCAAGAAGTGCTGTGAAGGCTC
 oProAsnArgCysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGlySe
 310 330 350
 TTGCGGGATGGCCTGTTTCGTTCCCCAGTGAGAGGGAGCCGGTCCTTGCTGCACCTGTGC
 rCysGlyMetAlaCysPheValProGlnEnd
 370 390 410
 CGTCCCCAGAGCTACAGGCCCCATCTGGTCCTAAGTCCCTGCTGCCCTTCCCCTTCCCAC
 430 450 470
 ACTGTCCATTCTTCCTCCCATTGAGGATGCCCACGGCTGGAGCTGCCTCTCTCATCCACT
 490
TTCCAATAAAGAGTTCCGGAATTC
 Poly A EcoRI
 signal

TDETHQ 66CEB00



pUEX2

EcoRI	SmaI	BamHI	SalI	PstI											
GAA	TTC	CCG	GGG	ATC	CGT	CGA	CCT	GCA	GCC	AAG	CTT	GCT	GAT	TGA	
Glu	Phe	Pro	Gly	Ile	Arg	Arg	Pro	Ala	Ala	Lys	Leu	Ala	Asp	***	

FIG 17

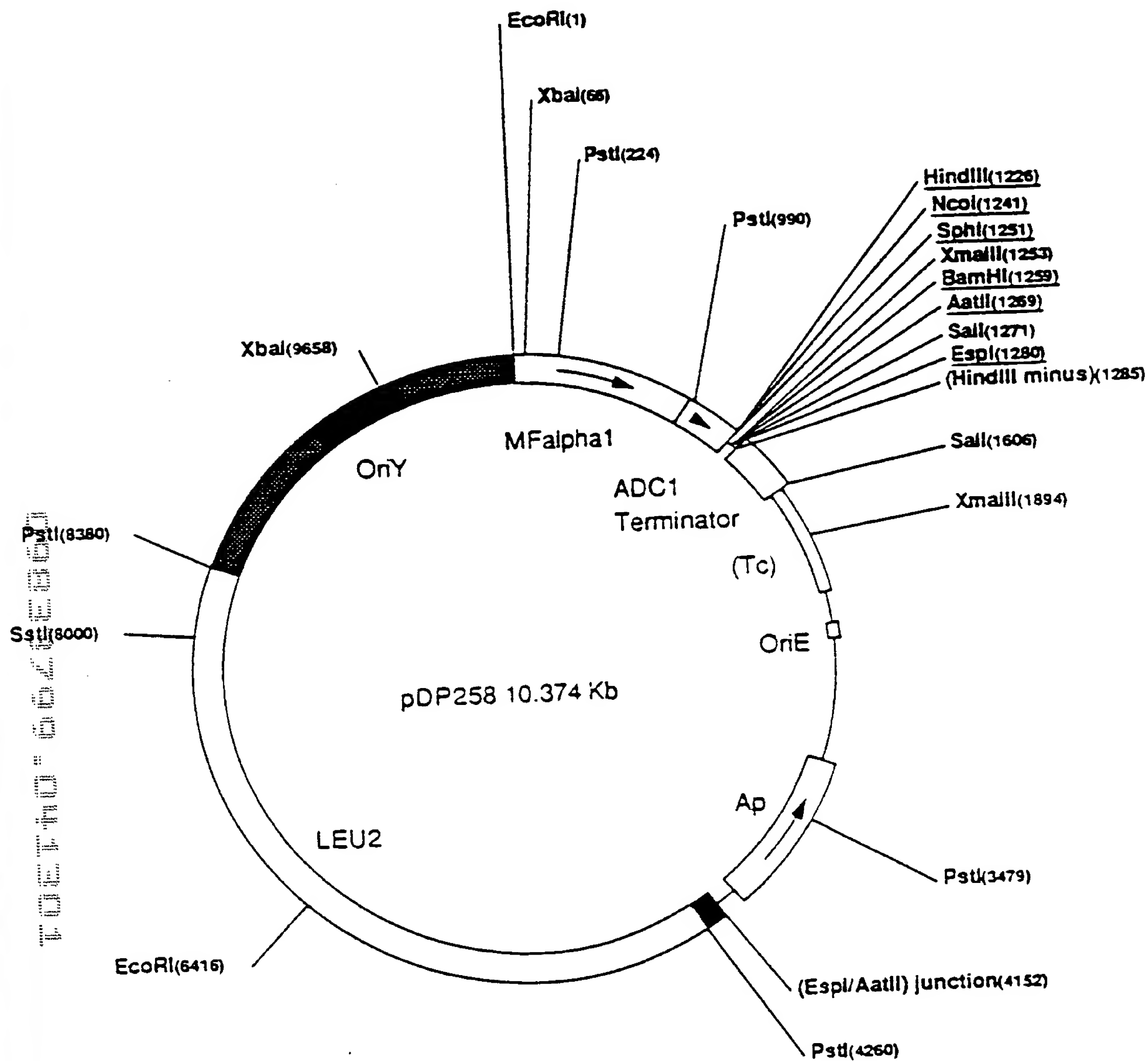


FIG 18

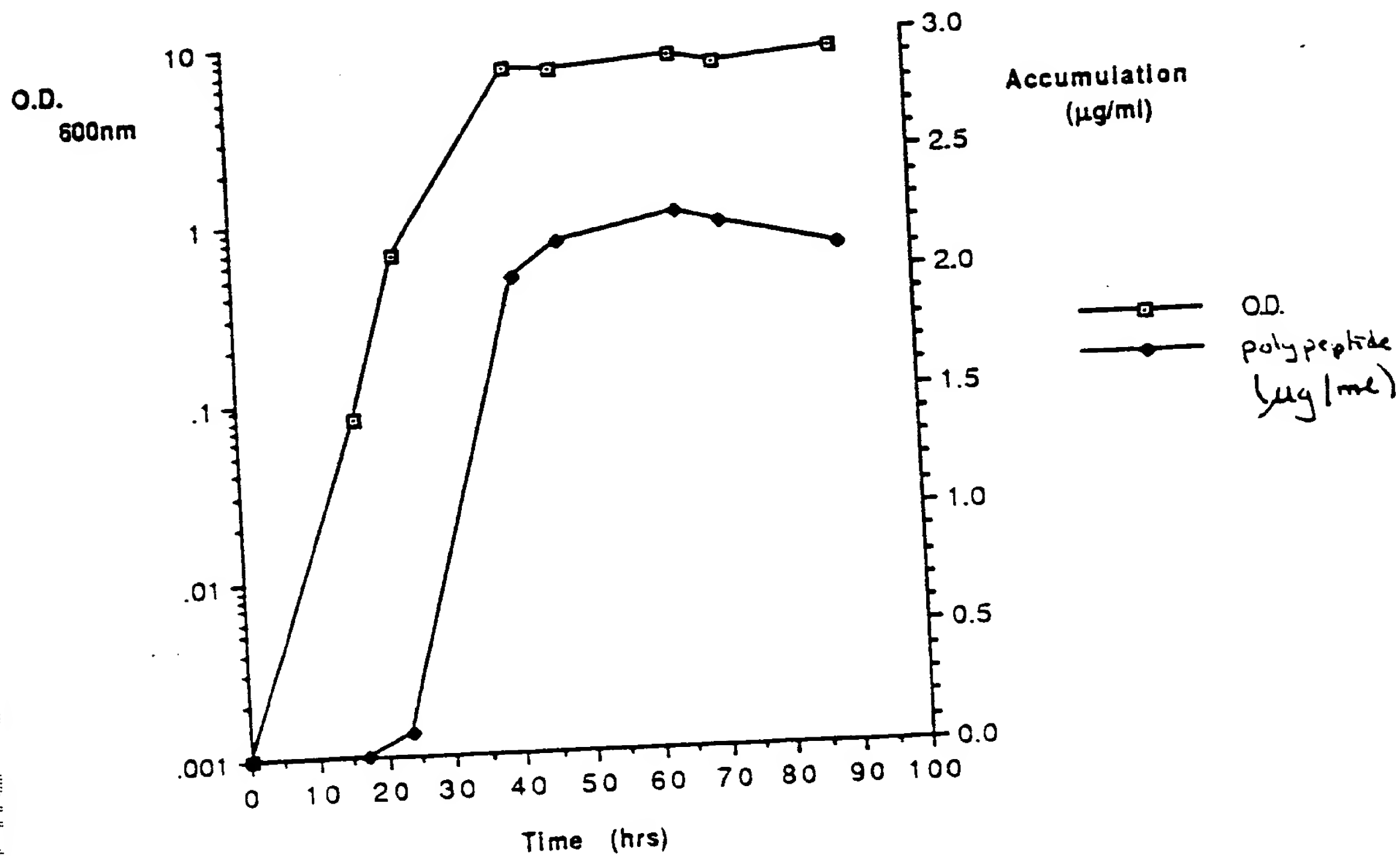


FIG 19